

1/49

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu-Ser
 65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255-

tac gct taa

Tyr Ala

777

<210> 2

<211> 258

<212> PRT

<213> Manihot esculenta

<400> 2

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

5

10

15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

4/49

tgc cca tct tac gtc gtg gat aag ctc atg gag gtg ttt ccc gac tgg 384
 Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp
 115 120 125

aaa gac acc acg tat ttt acg tac act aaa gat ggc aag gag ata-act 432
 Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr
 130 135 140

gga ttg aaa ctg ggc ttc acg ctt ctg agg gaa aat tta tat acc ctt 480
 Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu
 145 150 155 160

tgc ggt cct gag gaa tat gaa ctg gcg aag atg ttg aca agg aag gga 528
 Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly
 165 170 175

tca tta ttt caa aat att tta gct aag cga cca ttc ttc act aag gaa 576
 Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu
 180 185 190

ggt tac gga tcg att aag aaa att tat gtg tgg acc gac caa gac gaa 624
 Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu
 195 200 205

ata ttt tta cct gaa ttt caa ctc tgg caa ata gaa aac tat aaa cca 672
 Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro
 210 215 220

gac aag gtt tat aag gtc gaa ggt gga gat cat aaa ttg cag ctt aca 720
 Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr
 225 230 235 240

aag act aag gag atc gct gaa att ctc caa gag gtg gct gat acc tat 768
 Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr
 245 250 255

aat tga 774
 Asn

<210> 4

<211> 257

<212> PRT

<213> Hevea brasiliensis

<400> 4

Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile
 35 40 45
 Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser
 65 70 75 80
 Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys
 85 90 95
 Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His
 100 105 110
 Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp
 115 120 125
 Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr
 130 135 140
 Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu
 145 150 155 160
 Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly
 165 170 175
 Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu
 180 185 190
 Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu
 195 200 205
 Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro
 210 215 220
 Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr
 225 230 235 240
 Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr
 245 250 255
 Asn

<210> 5

<211> 777

<212> DNA

<213> *Manihot esculenta*

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Gly by Asp at position 165

<220>

<221> CDS

<222> (1).. (777)

<400> 5

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atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
  1           5           10          15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
      20           25           30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
      35           40           45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
      50           55           60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
      65           70           75           80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
      85           90           95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
      100          105          110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
      115          120          125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
      130          135          140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc aco 480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
      145          150          155          160

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aaa tgc act gat gac gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528
 Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777
 Tyr Ala

<210> 6
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>
 <223> Modified SHNL involving
 a replacement of Gly by Asp at position 165

<400> 6
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp-Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 Tyr Ala

<210> 7

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Gly by Glu at position 165

<400> 7

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His-Lys
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala-Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160

aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528
 Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180	185	190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac			624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp			
195	200	205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa			672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys			
210	215	220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg			720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu			
225	230	235	240
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca			768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala			
245	250	255	
tac gct taa			777
Tyr Ala			

<210> 8

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Gly by Glu at position 165

<400> 8

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala			
1	5	10	15
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys			
20	25	30	
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile			
35	40	45	
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe			
50	55	60	
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser			
65	70	75	80
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys			
85	90	95	
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His			

100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 Tyr Ala

<210> 9

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 9

ggggaattca tgggttactgc acacttcggtt ctgattcac

39

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 10

gggaagcttt taagcgtatg catcagcaac ttcttgcag

39

<210> 11

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 11

gggggggggc atatggttac tgcacacttc gttctgattc acac

44

<210> 12

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

gggggatcct taagcgtatg catcagcaac ttcttgacg

39

<210> 13

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 13

cgtgaaaacc tgttcaccaa atgcactgat gaagaatatg aactggcaaa aatg

54

<210> 14

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 14

catttttgcc agttcatatt cttcatcagt gcatttgggtg aacaggtttt cacg 54.

<210> 15

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1).. (777)

<220>

<223> cDNA coding for Modified SHNL involving
a replacement of Val by Leu at position 173

<400> 15

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100	105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg			384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp			
115	120	125	
cg t gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc			432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile			
130	135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cg t gaa aac ctg ttc acc			480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr			
145	150	155	160
aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg ctg atg cgc aag			528
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys			
165	170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cg t ccg aag ttc act gaa			576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu			
180	185	190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac			624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp			
195	200	205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa			672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys			
210	215	220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg			720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu			
225	230	235	240
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca			768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala			
245	250	255	
tac gct taa			777
Tyr Ala			

<210> 16

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving
a replacement of Val by Leu at position 173

<400> 16

Met	Val	Thr	Ala	His	Phe	Val	Leu	Ile	His	Thr	Ile	Cys	His	Gly	Ala	1	5	10	15
Trp	Ile	Trp	His	Lys	Leu	Lys	Pro	Ala	Leu	Glu	Arg	Ala	Gly	His	Lys	20	25	30	
Val	Thr	Ala	Leu	Asp	Met	Ala	Ala	Ser	Gly	Ile	Asp	Pro	Arg	Gln	Ile	35	40	45	
Glu	Gln	Ile	Asn	Ser	Phe	Asp	Glu	Tyr	Ser	Glu	Pro	Leu	Leu	Thr	Phe	50	55	60	
Leu	Glu	Lys	Leu	Pro	Gln	Gly	Glu	Lys	Val	Ile	Ile	Val	Gly	Glu	Ser	65	70	75	80
Cys	Ala	Gly	Leu	Asn	Ile	Ala	Ile	Ala	Ala	Asp	Arg	Tyr	Val	Asp	Lys	85	90	95	
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His	100	105	110	
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp	115	120	125	
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile	130	135	140	
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr	145	150	155	160
Lys	Cys	Thr	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Leu	Met	Arg	Lys	165	170	175	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu	180	185	190	
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp	195	200	205	
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys	210	215	220	
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu	225	230	235	240
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala	245	250	255	
Tyr	Ala																		

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 17

ggcgaatatg aactggcaaa aatgnnnatg cgcaagggt ctctg 45

<210> 18

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 18

cagagagccc ttgcgcatnn ncatttttgc cagttcatat tcgcc 45

<210> 19

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1).. (777)

<220>

<223> cDNA coding for Modified SHNL involving
a replacement of Met by Leu at position 174

<400> 19

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 agc ccg tct tac act gtt gaa aag ctg ctg gaa tcc ttc ccg gac tgg 384
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt ttg cgc aag 528
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys
 165 170 175
 ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 18/49

210	215	220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg			720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu			
225	230	235	-240
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca			768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala			
245	250	255	
tac gct taa			777
Tyr Ala			

<210> 20
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>
 <223> Modified SHNL involving
 a replacement of Met by Leu at position 174

<400> 20
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys

165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 Tyr Ala

<210> 21
 <211> 777
 <212> DNA
 <213> Manihot esculenta

<220>
 <221> CDS
 <222> -(1).. (777)

<220>
 <223> cDNA coding for Modified SHNL(SHNL Actmt022-G12) involving
 a replacement of Lys by Asn at position 21

<400> 21
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 tgg att tgg cac aat ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc	240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser	
65 70 75 80	
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac-aaa	288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys	
85 90 95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac	336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His	
100 105 110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tgc ttc ccg gac tgg	384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp	
115 120 125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc	432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile	
130 135 140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc	480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr	
145 150 155 160	
aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag	528
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys	
165 170 175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa	576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu	
180 185 190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac	624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp	
195 200 205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa	672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys	
210 215 220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg	720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu	
225 230 235 240	
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca	768
21/49	

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa
 Tyr Ala

777

<210> 22

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL(SHNL Actmt022-G12) involving
 a replacement of Lys by Asn at position 21

<400> 22

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

23/49

<400> 25

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15

tgg att tgg cac gaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa-gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777
 Tyr Ala

<210> 26

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving
 a replacement of Lys by Glu at position 21

<400> 26

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

	85		90		95										
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His
	100						105					110			
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp
	115						120					125			
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile
	130						135					140			
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr
	145						150				155			160	
Lys	Cys	Thr	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys
			165						170					175	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu
			180						185				190		
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp
			195					200					205		
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys
			210				215					220			
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu
	225				230					235				240	
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala
			245						250					255	

Tyr Ala

<210> 27
 <211> 777
 <212> DNA
 <213> Manihot esculenta

<220>
 <221> CDS
 <222> (1).. (777)

<220>
 <223> cDNA coding for Modified SHNL involving
 a replacement of Lys by Asp at position 21

<400> 27
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15

tgg att tgg cac gac ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Asp Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20	25	30	
gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att			144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile			
35	40	45	
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc			192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe			
50	55	60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc			240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser			
65	70	75	80
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa			288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys			
85	90	95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac			336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His			
100	105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg			384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp			
115	120	125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc			432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile			
130	135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc			480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr			
145	150	155	160
aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag			528
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys			
165	170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa			576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu			
180	185	190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac			624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp			
195	200	205	

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777
 Tyr Ala

<210> 28
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>
 <223> Modified SHNL involving
 a replacement of Lys by Asp at position 21

<400> 28
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Asp Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 Tyr Ala

<210> 29

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Lys by Asn at position 21

<400> 29

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15

tgg att tgg cac aac ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu	Gln	Ile	Asn	Ser	Phe	Asp	Glu	Tyr	Ser	Glu	Pro	Leu	Leu	Thr	Phe		
50						55				60							
ctg	gaa	aaa	ctg	ccg	caa	ggc	gaa	aag	gtt	atc	att	gtt	ggt	gaa	agc	240	
Leu	Glu	Lys	Leu	Pro	Gln	Gly	Glu	Lys	Val	Ile	Ile	Val	Gly	Glu	Ser		
65					70				75					80			
tgt	gca	ggc	ctg	aac	att	gct	att	gct	gct	gat	cgt	tac	gtt	gac	aaa	288	
Cys	Ala	Gly	Leu	Asn	Ile	Ala	Ile	Ala	Ala	Asp	Arg	Tyr	Val	Asp	Lys		
				85				90						95			
att	gca	gct	ggc	gtt	ttc	cac	aac	tcc	ctg	ctg	ccg	gac	acc	gtt	cac	336	
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His		
			100				105						110				
agc	ccg	tct	tac	act	gtt	gaa	aag	ctg	ctg	gaa	tgc	ttc	ccg	gac	tgg	384	
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp		
			115				120					125					
cgt	gac	aca	gaa	tat	ttc	acg	ttc	acc	aac	atc	act	ggc	gaa	acc	atc	432	
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile		
			130				135					140					
act	acc	atg	aaa	ctg	ggt	ttc	gtt	ctg	ctg	cgt	gaa	aac	ctg	ttc	acc	480	
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr		
			145				150			155				160			
aaa	tgc	act	gat	ggc	gaa	tat	gaa	ctg	gca	aaa	atg	gtt	atg	cgc	aag	528	
Lys	Cys	Thr	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys		
				165				170						175			
ggc	tct	ctg	ttc	caa	aac	gtt	ctg	gct	cag	cgt	ccg	aag	ttc	act	gaa	576	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu		
				180				185						190			
aaa	ggc	tac	ggc	tct	atc	aag	aaa	gtt	tat	att	tgg	acc	gat	caa	gac	624	
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp		
				195				200					205				
aaa	ata	ttc	ctg	ccg	gac	ttc	caa	cgc	tgg	caa	att	gca	aac	tac	aaa	672	
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys		
				210			215					220					
ccg	gac	aag	gtt	tat	cag	gtt	caa	ggc	ggc	gat	cac	aag	ctg	cag	ctg	720	
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu		

225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245 250 255~

tac gct taa 777

Tyr Ala

<210> 30

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving
a replacement of Lys by Asn at position 21

<400> 30

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195	200	205
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys		
210	215	220
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu		
225	230	235
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala		
245	250	255
Tyr Ala		

<210> 31

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1).. (777)

<220>

<223> cDNA coding for Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173

<400> 31

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca	48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala	

1

5

10

15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa	96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys	

20

25

30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att	144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile	

35

40

45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc	192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe	

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc	240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser	

65

70

75

80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa	288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys	
85 90 95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac	336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His	
100 105 110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg	384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp	
115 120 125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc	432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile	
130 135 140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc	480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr	
145 150 155 160	
aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg ctg atg cgc aag	528
Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys	
165 170 175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa	576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu	
180 185 190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac	624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp	
195 200 205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa	672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys	
210 215 220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg	720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu	
225 230 235 240	
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca	768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala	
245 250 255	
tac gct taa	777

Tyr Ala

<210> 32

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173

<400> 32

```

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1             5             10             15
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
          20             25             30
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
          35             40             45
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
          50             55             60
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
          65             70             75             80
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
          85             90             95
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
          100            105            110
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
          115            120            125
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
          130            135            140
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
          145            150            155            160
Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys
          165            170            175
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
          180            185            190
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
          195            200            205
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
          210            215            220
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
          225            230            235            240
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
          245            250            255

```

Tyr Ala

<210> 33

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 33

tatgaactgg caaaaatgct gctgcgcaag ggctctctgt tc

42

<210> 34

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 34

gaacagagag ccctigcgca gcagcatttt tgccagttca ta

42

<210> 35

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173
and Met by Leu at position 174

<400> 35

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1	5	10	15	
tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa				96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys				
20		25	30	
ggt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att				144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile				
35		40	45	
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc				192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe				
50		55	60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc				240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser				
65		70	75	80
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa				288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys				
85		90	95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac				336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His				
100		105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg				384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp				
115		120	125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc				432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile				
130		135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc				480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr				
145		150	155	160
aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg ctg ctg cgc aag				528
Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Leu Arg Lys				
165		170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa				576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu				
180		185	190	

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777
 Tyr Ala

<210> 36
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>
 <223> Modified SHNL involving
 replacement of Gly by Glu at position 165 and Val by Leu at position 173
 and Met by Leu at position 174

<400> 36
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Leu Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 Tyr Ala

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 37

tgaaaacctg ttacacaaat gcnngatgg cgaatatgaa ctggc

45

<210> 38

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 38

gccagttcat attgccatc nnngcatttg gtgaacaggt ttcca

45

<210> 39
 <211> 777
 <212> DNA
 <213> Manihot esculenta

<220>
 <223> cDNA coding for Modified SHNL involving
 a replacement of Thr by Asp at position 163

<220>
 <221> CDS
 <222> (1).. (777)
 <223>

<400> 39
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp		
	115						120					125					
cgt	gac	aca	gaa	tat	ttc	acg	ttc	acc	aac	atc	act	ggc	gaa	acc	atc	432	
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile		
	130					135					140						
act	acc	atg	aaa	ctg	ggt	ttc	gtt	ctg	ctg	cgt	gaa	aac	ctg	ttc	acc	480	
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr		
145					150					155				160			
aaa	tgc	gat	gat	ggc	gaa	tat	gaa	ctg	gca	aaa	atg	gtt	atg	cgc	aag	528	
Lys	Cys	Asp	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys		
				165					170					175			
ggc	tct	ctg	ttc	caa	aac	gtt	ctg	gct	cag	cgt	cgc	aag	ttc	act	gaa	576	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu		
		180						185					190				
aaa	ggc	tac	ggc	tct	atc	aag	aaa	gtt	tat	att	tgg	acc	gat	caa	gac	624	
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp		
	195					200					205						
aaa	ata	ttc	ctg	cgc	gac	ttc	caa	cgc	tgg	caa	att	gca	aac	tac	aaa	672	
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys		
	210					215					220						
cgc	gac	aag	gtt	tat	cag	gtt	caa	ggc	ggc	gat	cac	aag	ctg	cag	ctg	720	
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu		
225					230					235				240			
aca	aaa	act	gaa	gaa	gta	gct	cac	att	ctg	caa	gaa	gtt	gct	gat	gca	768	
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala		
			245						250					255			
tac	gct	taa														777	
Tyr	Ala																

<210> 40
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>

<223> Modified SHNL involving
a replacement of Thr by Asp at position 163

<400> 40

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
145 150 155 160

Lys Cys Asp Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

Tyr Ala

<210> 41
 <211> 777
 <212> DNA
 <213> Manihot esculenta

<220>
 <223> cDNA coding for Modified SHNL involving
 a replacement of Thr by Glu at position 163

<220>
 <221> CDS
 <222> (1).. (777)
 <223>

<400> 41
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

43/49

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
145 150 155 160

Lys Cys Glu Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp-Ala
 245 250 255

Tyr Ala

<210> 43

<211> 777

<212> DNA

<213> *Manihot esculenta*

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Thr by Ser at position 163

<220>

<221> CDS

<222> (1).. (777)

<223>

<400> 43

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65	70	75	80	
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa				288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys				
85		90	95 -	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac				336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His				
100	105		110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tgc ttc ccg gac tgg				384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp				
115	120		125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc				432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile				
130	135		140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc				480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr				
145	150	155	160	
aaa tgc tct gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag				528
Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys				
165	170		175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa				576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu				
180	185		190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac				624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp				
195	200		205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa				672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys				
210	215		220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg				720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu				
225	230	235	240	
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca				768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala				
245	250		255	

tac gct taa
Tyr Ala

777

<210> 44
<211> 258
<212> PRT
<213> Manihot esculenta

<220>
<223> Modified SHNL involving
a replacement of Thr by Ser at position 163

<400> 44

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
145 150 155 160

Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
245 250 255

Tyr Ala